

RAW SEQUENCE LISTING

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Application Serial Number: 10/523,328
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DATE: 10/05/2005

PATENT APPLICATION: US/10/523,328

TIME: 16:05:40

Input Set : A:\WYTH-P01-001 seq.txt

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3 <110> APPLICANT: Kuai, Jun
4     Lin, Lih-Ling
5     Wooters, Joseph L.
6     Nickbarg, Elliot
8 <120> TITLE OF INVENTION: METHODS AND REAGENTS RELATING TO INFLAMMATION AND APOPTOSIS
10 <130> FILE REFERENCE: WYTH-P01-001
12 <140> CURRENT APPLICATION NUMBER: US 10/523,328
13 <141> CURRENT FILING DATE: 2005-02-01
15 <150> PRIOR APPLICATION NUMBER: 60/400,410
16 <151> PRIOR FILING DATE: 2002-08-01
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 233
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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30 1          5          10          15
33 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
34          20          25          30
37 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
38          35          40          45
41 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
42          50          55          60
45 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
46 65          70          75          80
49 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
50          85          90          95
53 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
54          100         105         110
57 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
58          115         120         125
61 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
62          130         135         140
65 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
66 145         150         155         160
69 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
70          165         170         175
73 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
74          180         185         190
77 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
78          195         200         205

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81 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
82      210                      215                      220
85 Gln Val Tyr Phe Gly Ile Ile Ala Leu
86 225                      230
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90 <211> LENGTH: 701
91 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 2
95 atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct cccaagaag      60
97 acaggggggc ccagggctcc aggcggtgct tgttcctcag cctcttctcc ttcctgatcg      120
99 tggcaggcgc caccacgctc ttctgcctgc tgcactttgg agtgatcggc cccagagggg      180
101 aagagttccc cagggacctc tctctaata ggcctctggc ccaggcagtc agatcatctt      240
103 ctcgaacccc gagtgacaag cctgtagccc atgttgtagc aaacctcaa gctgaggggc      300
105 agctccagtg gctgaaccgc cgggccaatg ccctcctggc caatggcgtg gagctgagag      360
107 ataaccagct ggtggtgcca tcagagggcc tgtacctcat ctactcccag gtcctcttca      420
109 agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc cgcacgccc      480
111 tctcctacca gaccaaggtc aacctcctct ctgccatcaa gagcccctgc cagagggaga      540
113 cccagagggg ggctgaggcc aagccctggt atgagcccat ctatctggga ggggtcttcc      600
115 agctggagaa gggtgaccga ctacgcgctg agatcaatcg gcccgactat ctgcactttg      660
117 ccgagtcctg gcagggtctac tttgggatca ttgccctgtg a                      701
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121 <211> LENGTH: 455
122 <212> TYPE: PRT
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 3
127 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
128 1                      5                      10                      15
131 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
132      20                      25                      30
135 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
136      35                      40                      45
139 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
140      50                      55                      60
143 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
144 65                      70                      75                      80
147 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
148      85                      90                      95
151 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
152      100                     105                     110
155 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
156      115                     120                     125
159 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
160      130                     135                     140
163 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
164 145                     150                     155                     160
167 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
168      165                     170                     175
171 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr

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175 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
176          195          200          205
179 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
180          210          215          220
183 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
184 225          230          235          240
187 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
188          245          250          255
191 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
192          260          265          270
195 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
196          275          280          285
199 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
200          290          295          300
203 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
204 305          310          315          320
207 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
208          325          330          335
211 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
212          340          345          350
215 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
216          355          360          365
219 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
220          370          375          380
223 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
224 385          390          395          400
227 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
228          405          410          415
231 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
232          420          425          430
235 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
236          435          440          445
239 Pro Ala Pro Ser Leu Leu Arg
240          450          455
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244 <211> LENGTH: 1367
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 4
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251 ggaatatacc cctcaggggt tattggactg gtccctcacc taggggacag ggagaagaga      120
253 gatagtgtgt gtcccaagg aaaatatatc caccctcaaa ataattcgat ttgctgtacc      180
255 aagtgccaca aaggaacctt cttgtacaat gactgtccag gcccggggca ggatacggac      240
257 tgacaggagt gtgagagcgt ctcttcacc gcttcagaaa accacctcag acactgcctc      300
259 agctgctcca aatgccgaaa ggaaatgggt caggtggaga tctcttcttg cacagtggac      360
261 cgggacaccg tgtgtggctg caggaagaac cagtaccggc attattggag tgaaaacctt      420
263 ttccagtgtc tcaattgcag cctctgcctc aatgggaccg tgcacctctc ctgccaggag      480
265 aaacagaaca ccgtgtgcac ctgccatgca ggtttctttc taagagaaaa cgagtgtgtc      540

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267 tcctgtagta actgtaagaa aagcctggag tgcacgaagt tgtgcctacc ccagattgag      600
269 aatgttaagg gcactgagga ctcaggcacc acagtgtgtg tgcccctggg cattttcttt      660
271 ggtctttgcc ttttatccct cctcttcatt ggtttaatgt atcgctacca acggtggaag      720
273 tccaagctct actccattgt ttgtgggaaa tgcacacctg aaaaagaggg ggagcttgaa      780
275 ggaactacta ctaagcccct ggcccaaac ccaagcttca gtccactcc aggcttcacc      840
277 cccaccctgg gcttcagtc cgtgcccagt tccaccttca cctccagctc cacctatacc      900
279 cccggtgact gtcccaactt tgcggtcccc cgcagagagg tggcaccacc ctatcagggg      960
281 gctgacccca tccttgcgac agccctcgcc tccgaccca tcccaacccc cttcagaagt     1020
283 gggaggacag cgcccacaag ccacagagcc tagacactga tgaccccgcg acgctgtacg     1080
285 ccgtggtgga gaacgtgccc ccgttgcgct ggaaggaatt cgtgcggcgc ctagggtga     1140
287 gcgaccacga gatcgatcgg ctggagctgc agaacgggcg ctgcctgcgc gaggcgcaat     1200
289 acagcatgct ggcgacctgg aggcggcgca cgccgcgcg cgaggccacg ctggagctgc     1260
291 tgggacgcgt gtcgccgcac atggacctgc tgggctgcct ggaggacatc gaggagggcg     1320
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297 <211> LENGTH: 461
298 <212> TYPE: PRT
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 5
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304 1 5 10 15
307 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
308 20 25 30
311 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
312 35 40 45
315 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
316 50 55 60
319 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
320 65 70 75 80
323 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
324 85 90 95
327 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
328 100 105 110
331 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
332 115 120 125
335 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
336 130 135 140
339 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
340 145 150 155 160
343 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
344 165 170 175
347 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
348 180 185 190
351 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
352 195 200 205
355 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
356 210 215 220
359 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
360 225 230 235 240

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363 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
364           245           250           255
367 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
368           260           265           270
371 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
372           275           280           285
375 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
376           290           295           300
379 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
380 305           310           315           320
383 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
384           325           330           335
387 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
388           340           345           350
391 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
392           355           360           365
395 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
396           370           375           380
399 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
400 385           390           395           400
403 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
404           405           410           415
407 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
408           420           425           430
411 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
412           435           440           445
415 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
416           450           455           460

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419 <210> SEQ ID NO: 6

420 <211> LENGTH: 1384

421 <212> TYPE: DNA

422 <213> ORGANISM: Homo sapiens

424 <400> SEQUENCE: 6

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425 atggcgcccg tcgccgtctg gccgcgctg gccgtcggac tggagctctg ggctgcggcg      60
427 cagccttgcc ccgccaggt ggcatttaca ccctacgcc cggagcccg gagcacatgc      120
429 cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctgccggggc      180
431 caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac      240
433 agcacataca ccagctctg gaactgggtt cccgagtgtg tgagctgtgg ctcccgtgtg      300
435 agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc      360
437 agggccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgtg      420
439 cgcaagtgcc gcccggtt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg      480
441 tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg      540
443 cccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc      600
445 acgtccacgt cccccacccg gagtatggcc caggggcagt acacttacct cagccagtgt      660
447 ccacacgata ccaacacacg cagccaactc cagaacccag cactgtctcca agcacctcct      720
449 tcctgtctcc aatgggcccc agccccagc tgaagggagc actggcgact tcgctcttcc      780
451 agttggactg attgtgggtg tgacagcctt ggggtctacta ataataggag tggtgaactg      840
453 tgtcatcatg acccaggtga aaaagaagcc cttgtgcctg cagagagaag ccaaggtgcc      900
455 tcacttgccg gccgataagg cccgggttac acaggggccc gagcagcagc acctgctgat      960

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VERIFICATION SUMMARY

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